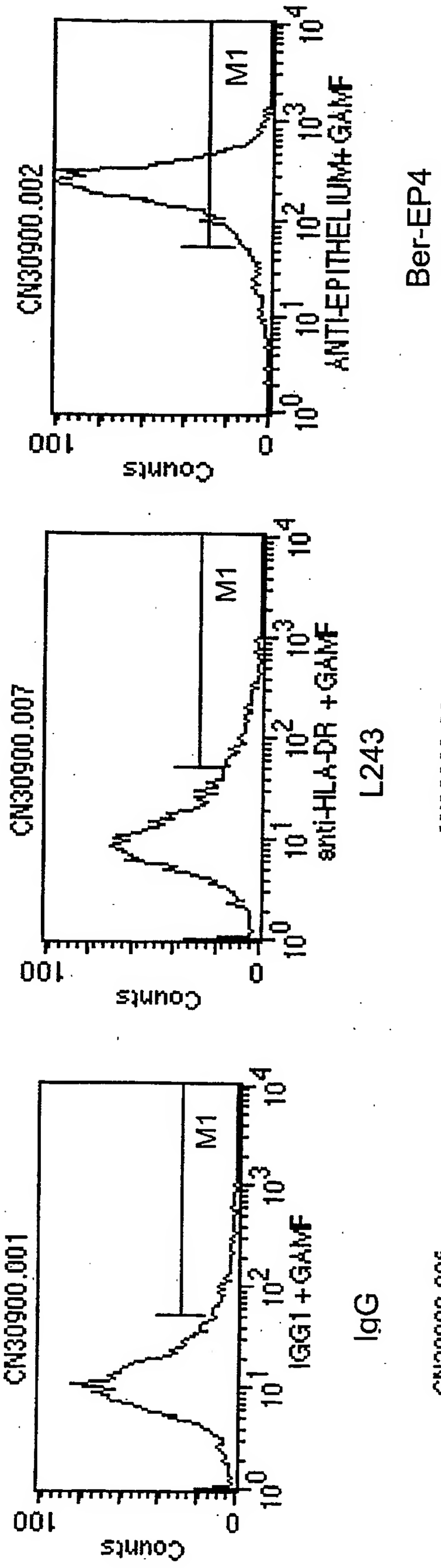
CN30900.002
M1
ANTI-EPITHELIUM+GAMF
Counts
100
0
Ber-EP4
CN30900.007
M1
anti-HLA-DR +GAMF
Counts
100
0
L243
CN30900.003
M1
ANTI-FIBROBLAST+GAMF
Counts
100
0
5B5
CN30900.001
M1
IGG1+GAMF
Counts
100
0
IgG
CN30900.006
M1
W 6/32 FITC
Counts
100
0
W6/32

FIG. 1A

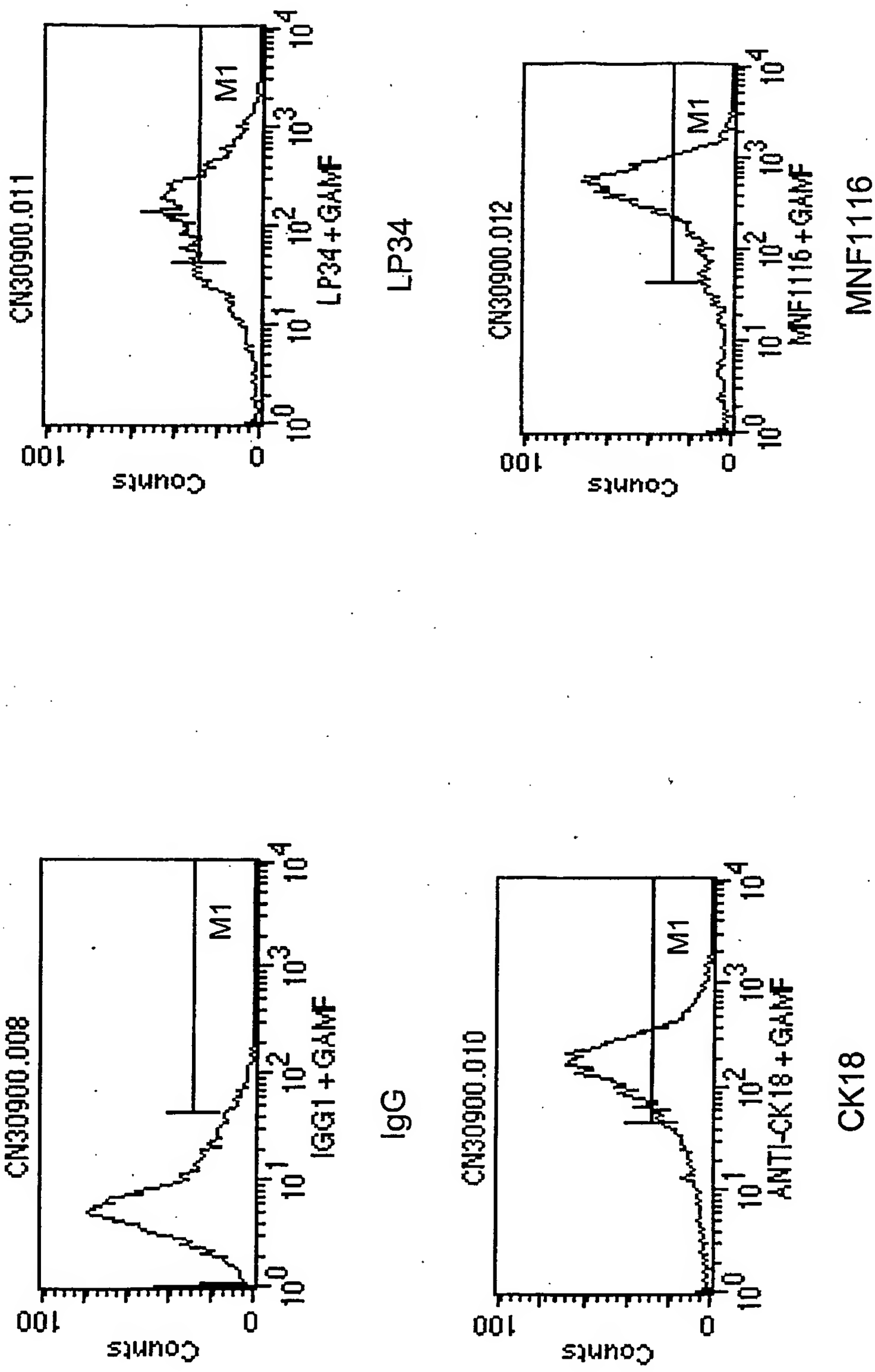
CN30900.011
M1
LP34+GAMF
LP34
CN30900.012
M1
MNF1116+GAMF
MNF1116
CN30900.008
M1
IGG1+GAMF
IgG
CN30900.010
M1
ANTI-CK18+GAMF
CK18
Counts
100
0

FIG. 1B

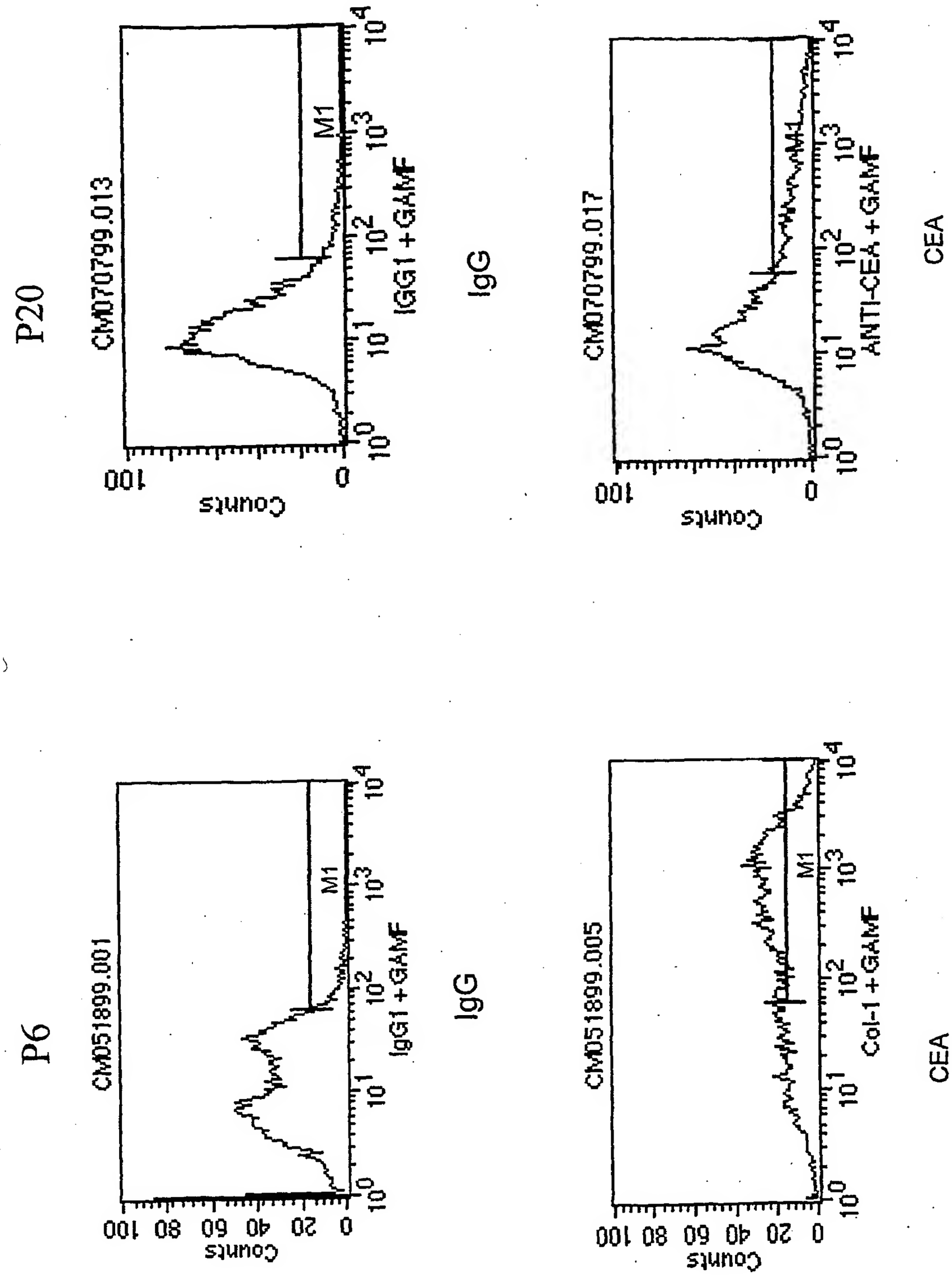
P20
CM070799.013
M1
IGG1+GAMF
IgG
CM070799.017
ANTI-CEA+GAMF
CEA
P6
CM051899.001
M1
IgG1+GAMF
IgG
CM051899.005
M1
Col-1+GAMF
CEA
Counts
0
100
0 20 40 60 80 100

FIG 1C

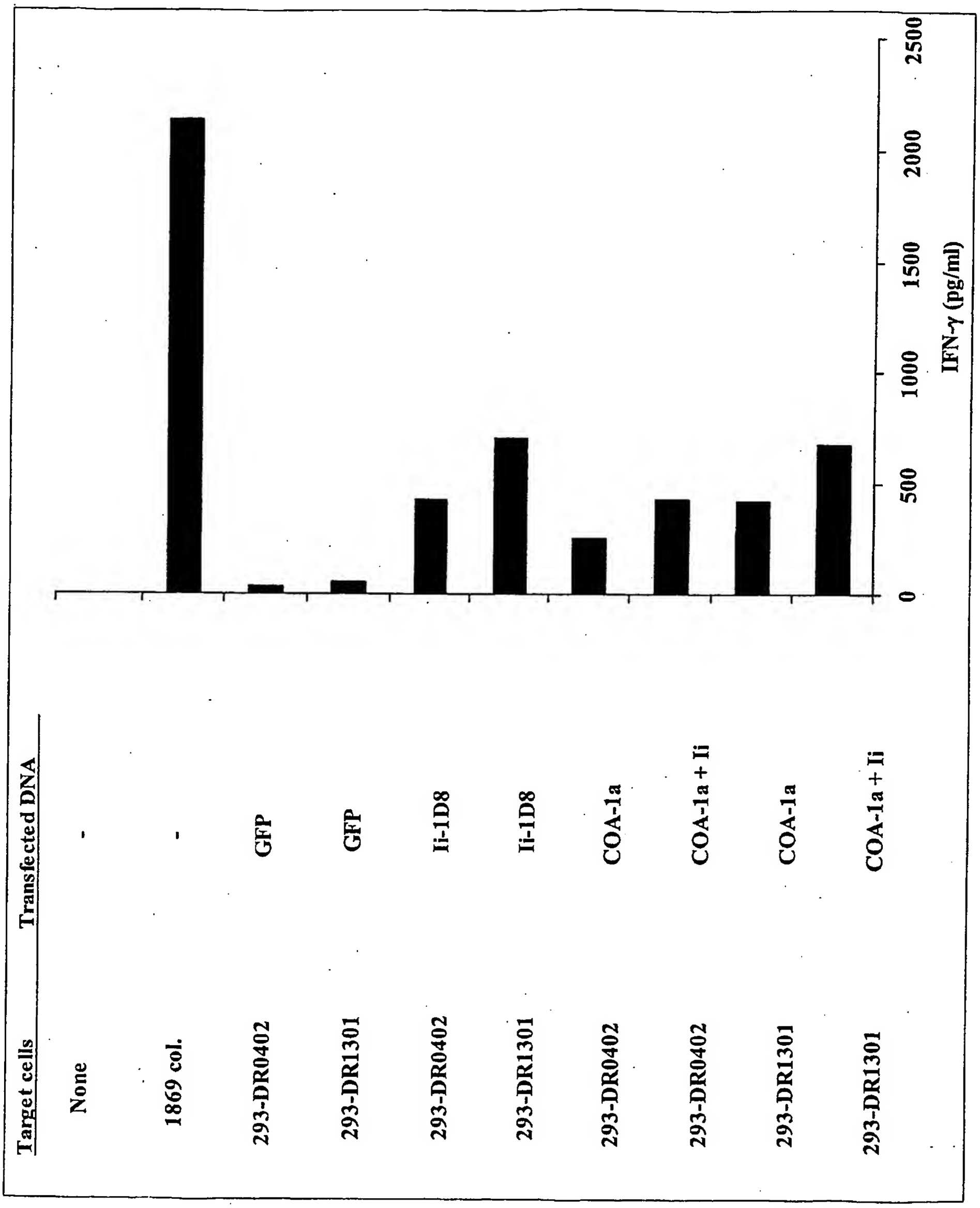
IFN-γ (pg/ml)
0
500
1000
1500
2000
2500
Transfected DNA
-
-
GFP
GFP
Ii-1D8
Ii-1D8
COA-1a
COA-1a + Ii
COA-1a
COA-1a + Ii
Target cells
None
1869 col.
293-DR0402
293-DR1301
293-DR0402
293-DR1301
293-DR0402
293-DR0402
293-DR1301
293-DR1301

FIG. 2

```
MAFMTRKLWD LEQQVKAQTD EILSKDQKIA ALEDLVQTLR PHPAEATLQR QEELETMCVQ  60
LQRQVREMER FLSDYGLQWV GEPMDQEDSE SKTVSEHGER DWMTAKKFWK PGDSLAPPEV 120
DFDRLLASLQ DLSELVVEGD TQVTPVPGGA RLRTLEPIPL KLYRNGIMMF DGPFQPFYDP 180
STQRCLRDIL DGFFPSELQR LYPNGVPFKV SDLRNQVYLE DGLDPFPGEG RVVGRQRMHK 240
ALDRVEEHPG SRMTAEKFLN RLPKFVIRQG EVIDIRGPIR DTLQNCCPLP ARIQEIVVET 300
PTLAAERERS QESPNTPAPP LSMLRIKSEN GEQAFLLMMQ PDNTIGDVRA LLAQARVMDA 360
SAFEIFSTFP PTLYQDDTLT LQAAGLVPKA ALLLRARRAP KSSLKFSPGP CPGPGPGPSP 420
GPGPGSSPCP GPSPSPQ                                               437
```

Alanine at position 399

FIG. 3

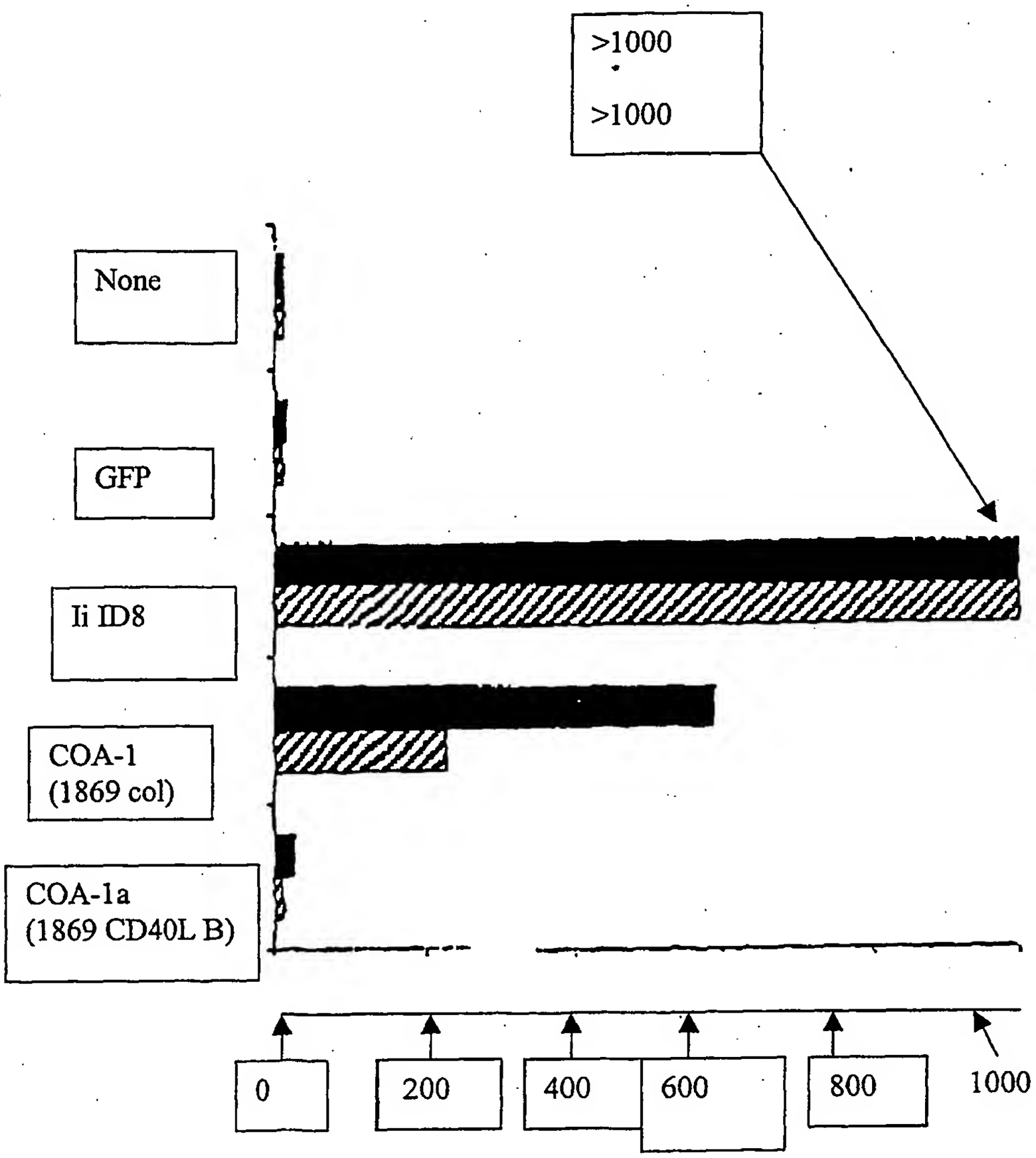
>1000
>1000
None
GFP
Ii ID8
COA-1
(1869 col)
COA-1a
(1869 CD40L B)
0
200
400
600
800
1000
IFN-γ (pg/ml)

FIG. 4

```
cgctgcggga cggctagcgg ccctgcgtgg aggcgaggaa tccgcatcta tggagatgtc  60

cctgcatccc atgactcgga gctg atg gcc ttc atg acg agg aag ttg tgg    111
                          Met Ala Phe Met Thr Arg Lys Leu Trp
                          1               5

gac ctg gag cag cag gtg aag gcc cag act gat gag ata ctg tcc aag   159
Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu Ile Leu Ser Lys
10                  15                  20                  25

gat cag aag ata gcg gcc cta gag gac ctg gtg cag acc ctc cgg cca   207
Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln Thr Leu Arg Pro
                30                  35                  40

cac cca gcc gag gca acc ctg cag cgg cag gag gaa ctg gag acg atg   255
His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu Leu Glu Thr Met
            45                  50                  55

tgt gtg cag ctg cag cgg cag gtc agg gag atg gag cgg ttc ctc agt   303
Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu Arg Phe Leu Ser
        60                  65                  70

gac tat ggc ctg cag tgg gtg ggc gag ccc atg gac cag gag gac tca   351
Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp Gln Glu Asp Ser
    75                  80                  85

gag agc aag aca gtc tca gag cat ggc gag agg gac tgg atg aca gcc   399
Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp Trp Met Thr Ala
90                  95                  100                 105

aag aag ttc tgg aag cca ggg gac tca ttg gcg ccc cct gag gtg gac   447
Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu Val Asp
                110                 115                 120

ttt gac agg ctg ctg gcc agc ctg cag gat ctt agt gag ctg gtg gta   495
Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu Val Val
            125                 130                 135

gag ggt gac acc caa gtg aca cca gtg ccc ggc ggg gca cgg ctg cgt   543
Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg Leu Arg
        140                 145                 150

acc ctc gag ccc atc ccg ctg aag ctc tac cgg aat ggc atc atg atg   591
Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile Met Met
    155                 160                 165

ttc gac ggg ccc ttc cag ccc ttc tac gat ccc tcc aca cag cgc tgc   639
Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln Arg Cys
170                 175                 180                 185

ctc cga gac ata ttg gat ggc ttc ttt ccc tca gag ctc cag cga ctg   687
Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln Arg Leu
                190                 195                 200

tac ccc aat ggg gtc ccc ttt aag gtg agt gac ttg cgc aat cag gtc   735
Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn Gln Val
            205                 210                 215
```

FIG. 5

```
tac ctg gag gat gga ctg gac ccc ttc cca ggc gag ggc cgt gtg gtg   783
Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg Val Val
        220                 225                 230

ggc agg cag cgg atg cac aag gcc ttg gac agg gtg gag gag cac cca   831
Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu His Pro
    235                 240                 245

ggc tcc agg atg act gct gag aaa ttt ctg aac agg ctc ccc aag ttt   879
Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro Lys Phe
250                 255                 260                 265

gtg atc cgg caa ggc gag gtg att gac atc cgg ggc ccc atc agg gac   927
Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile Arg Asp
                270                 275                 280

acc ttg cag aac tgc tgc cca ttg cct gcc cgg atc cag gag att gtg   975
Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu Ile Val
            285                 290                 295

gtg gag acg ccc acc ttg gcc gct gag cga gag agg agc cag gag tca  1023
Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln Glu Ser
        300                 305                 310

ccc aac aca ccg gca ccc ccg ctc tcc atg ctg cgc atc aag tct gag  1071
Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys Ser Glu
    315                 320                 325

aat ggg gaa cag gcc ttc cta ctg atg atg cag cct gac aac acc att  1119
Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn Thr Ile
330                 335                 340                 345

ggg gac gtg cga gct ctg cta gcg cag gcc agg gtc atg gat gcc tct  1167
Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp Ala Ser
                350                 355                 360

gcc ttt gag atc ttc agc aca ttc ccg ccc acc ctc tac cag gac gat  1215
Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp
            365                 370                 375

aca ctc acg ctg cag gct gca ggc ctt gtg ccc aaa gca gca ctg ctg  1263
Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala Leu Leu
        380                 385                 390
```

Cytosine at position 1280

```
ctg cgg gca cgc cga gCc ccg aag tcc agc ctg aaa ttc agt cct ggt
1311
Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly
    395                 400                 405
```

Alanine at position 399

```
ccc tgt ccc ggt ccc ggt ccc ggc ccc agt ccc ggt ccc ggt ccc ggc  1359
Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly
410                 415                 420                 425
```

FIG. 5 cont.

```
tcc agt ccc tgt ccc gga ccc agt ccc agc ccc caa taaagcaccc       1405
Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
                430                 435

acccccctc                                                       1413
```

FIG. 5 cont.